



SEQUENCE LISTING

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Mach, Bernard

<120> NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES,
SUBSTANCES CAPABLE OF INHIBITING THIS NEW
TRANSCRIPTION FACTOR AND MEDICAL USES OF THESE SUBSTANCES

<130> 23135-510 CON

<140> 09/840,243

<141> 2001-04-24

<150> EP 98120085.0

<151> 1998-10-24

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 1

ccgtacgcgt ctagaccatg gagcttacc agcctgcaga

40

<210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 2

ttcgaattct cgagtgtctg agtccccggc a

31

<210> 3

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 3

ccgtacgcgt ctagaccatg gagccactc aggttgc

37

<210> 4

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 4

ttcgaattct cgagtgcttg gggtccagca gg

32

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 5

ccagctctag actccaccac tctcaccaac

30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 6

ccttcgaatt ctcgctcttt tgccaggatg

30

<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 7

ggttctctag attggcagca ctggggatag

30

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 8

gctacgaatt ccagcagaca cagccaaaac

30

<210> 9

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 9

ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct tacccagcct 60

gcagaagac

69

<210> 10

<211> 1345

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (418)..(1200)

<400> 10

acgcagggaa ggaggcacac ccgggggtgg cgcagtgagg agggggcgcg acggccagga 60

ggctgggtgga ggcacaccca ggcaggagag ggggaagaac tctctccctt tctgaacccc 120

cttttccttg agagacgagt tgggggagtc ctccacgcat taccactcg ggccgcaaaa 180

actcccttct ttagccctct gccccgccc ttgcttataa gcctttgaga ccgcagaagg 240

gaccttggtg tggaacggga cggccaagag gaagccagat cgctgagggt ccggtctcca 300

gtttgcctcc tgctatatcc attggaagag aaaagtttgt gacttgggcc cccaagtttt 360

gagagaactg ggctttcggc gcggggggac agaggaggct cgtggggagc tttcccc 417

atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc 465

Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr

1

5

10

15

cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca 513

Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala

20

25

30

gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag 561

Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu

35

40

45

cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc 609

Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly

50

55

60

agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac 657

Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn

65

70

75

80

gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag 705

Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln

85

90

95

ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa 753

Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys

100

105

110

ggt gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc 801
 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
 115 120 125

atc tgg gcc tcc gcc ttt gga gag att gag acc gtt cgc ttc ctg ctg 849
 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
 130 135 140

gag tgg ggt gcc gac ccc cac atc ctg gca aaa gag cga gag agc gcc 897
 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
 145 150 155 160

ctg tcg ctg gcc agc aca ggc ggc tac aca gac att gtg ggg ctg ctg 945
 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
 165 170 175

ctg gag cgt gac gtg gac atc aac atc tat gat tgg aat gga ggg acg 993
 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
 180 185 190

cca ctg ctg tac gct gtg cgc ggc aac cac gtg aaa tgc gtt gag gcc 1041
 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
 195 200 205

ttg ctg gcc cga ggc gct gac ctc acc acc gaa gcc gac tct ggc tac 1089
 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
 210 215 220

acc ccg atg gac ctt gcc gtg gcc ctg gga tac cgg aaa gtg caa cag 1137
 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
 225 230 235 240

gtg atc gag aac cac atc ctc aag ctc ttc cag agc aac ctg gtg ccc 1185
 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
 245 250 255

gct gac cct gag tga aggccgctg ccgggggactc agacactcag ggaacaaaat 1240
 Ala Asp Pro Glu
 260

ggtcagccag agctgggggaa acccagaact gacttcaaag gcagcttctg gacaggtggt 1300

gggagggggac ccttcccaag aggaaccaat aaaccttctg tgcag 1345

<210> 11
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
 1 5 10 15
 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
 20 25 30
 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
 35 40 45

Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
 50 55 60
 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
 65 70 75 80
 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
 85 90 95
 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
 100 105 110
 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
 115 120 125
 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
 130 135 140
 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
 145 150 155 160
 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
 165 170 175
 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
 180 185 190
 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
 195 200 205
 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
 210 215 220
 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
 225 230 235 240
 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
 245 250 255
 Ala Asp Pro Glu
 260

<210> 12
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
 1 5 10 15
 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
 20 25 30

Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
 35 40 45
 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
 50 55 60
 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
 65 70 75 80
 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
 85 90 95
 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
 100 105 110
 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
 115 120 125
 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
 130 135 140
 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
 145 150 155 160
 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
 165 170 175
 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
 180 185 190
 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
 195 200 205
 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
 210 215 220
 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
 225 230 235 240
 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
 245 250 255
 Ala Asp Pro Glu
 260

<210> 13
 <211> 269
 <212> PRT
 <213> Murinae gen. sp.

<400> 13
 Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro
 1 5 10 15
 Pro Val Pro Asp Leu Glu Asp Pro Glu Asp Thr Arg Asp Glu Ser Pro
 20 25 30
 Glu Asn Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Asp
 35 40 45

Ala Val Asn Pro Glu Ala Asp Ala Ser Ala Ser Ser Leu Gln Gly Ser
50 55 60

Phe Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn Glu
65 70 75 80

Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln Leu
85 90 95

Ala Ala Gln Gly Glu Leu Ser Gln Leu Lys Asp His Leu Arg Lys Gly
100 105 110

Ala Cys Pro Ala Cys Thr Cys Leu Ser Gly Asn Asn Leu Ile Asn Lys
115 120 125

Pro Asp Glu Arg Gly Phe Thr Pro Leu Ile Trp Ala Ser Ala Phe Gly
130 135 140

Glu Ile Glu Thr Val Arg Phe Leu Leu Asp Trp Gly Ala Asp Pro His
145 150 155 160

Ile Leu Ala Lys Glu Arg Glu Ser Ala Leu Ser Leu Ala Ser Met Gly
165 170 175

Gly Tyr Thr Asp Ile Val Arg Leu Leu Leu Asp Arg Asp Val Asp Ile
180 185 190

Asn Ile Tyr Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val Arg
195 200 205

Gly Asn His Val Lys Cys Val Glu Ala Leu Leu Ala Arg Gly Ala Asp
210 215 220

Leu Thr Thr Glu Ala Asp Ser Gly Tyr Thr Pro Met Asp Leu Ala Val
225 230 235 240

Ala Leu Gly Tyr Arg Lys Val Gln Gln Val Met Glu Ser His Ile Leu
245 250 255

Arg Leu Phe Gln Ser Thr Leu Gly Pro Val Asp Pro Glu
260 265

<210> 14
<211> 111
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(111)

<400> 14
acc cta gac tgg tgc cga ccc cca cat cct ggc aaa aga gcg aga gag 48
Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu
1 5 10 15

cgc cct gtc gct ggc cag cac agg cgg cta cac aga cat tgt ggg gct 96
Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala
20 25 30

gct gct gga gcg tga
 Ala Ala Gly Ala
 35

111

<210> 15
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 15
 Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu
 1 5 10 15

Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala
 20 25 30

Ala Ala Gly Ala
 35

<210> 16
 <211> 42
 <212> DNA
 <213> Homo sapiens

<220>
 <221> exon
 <222> (31)..(42)

<400> 16
 ctggtggtat tgcccgcctc ctctgccag gtg aca acc tcg

42

<210> 17
 <211> 74
 <212> DNA
 <213> Homo sapiens

<220>
 <221> exon
 <222> (1)..(27)

<400> 17
 gag acc gtt cgc ttc ctg ctg gag tgg gtgcgtccca gccagctgg

47

gcagctgggg ggttcccggg ggcctta

74

<210> 18
 <211> 220
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (31)
 <223> wherein Xaa is any amino acid

<220>
 <221> MISC_FEATURE

<222> (148)
<223> wherein Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (159)
<223> wherein Xaa is any amino acid

<400> 18
Asn Ala Phe Asn Val Phe Thr Phe Val Phe His Leu Ala Glu Cys Asn
1 5 10 15
Ile His Thr Ser Pro Ser Pro Gly Ile Gln Val Arg His Val Xaa Thr
20 25 30
Pro Ser Thr Thr Lys His Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu
35 40 45
Thr Asn Lys His Arg Gly Asn Glu Val Ser Thr Thr Pro Leu Leu Ala
50 55 60
Asn Ser Leu Ser Val His Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr
65 70 75 80
Leu Ala Thr Arg Ile Glu Gln Glu Asn Val Ile Asn His Thr Asp Glu
85 90 95
Glu Gly Phe Thr Pro Leu Met Trp Ala Ala Ala His Gly Gln Ile Ala
100 105 110
Val Val Glu Phe Leu Leu Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly
115 120 125
Lys Gly Arg Glu Ser Ala Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr
130 135 140
Asp Ile Val Xaa Met Leu Leu Asp Cys Gly Val Asp Val Asn Xaa Tyr
145 150 155 160
Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val His Gly Asn His
165 170 175
Val Lys Cys Val Lys Met Leu Leu Glu Ser Gly Ala Asp Pro Thr Ile
180 185 190
Glu Thr Asp Ser Gly Tyr Asn Ser Met Asp Leu Ala Val Ala Leu Gly
195 200 205
Ile Glu Val Phe Asn Arg Leu Leu Ser His Ile Cys
210 215 220

<210> 19
<211> 218
<212> PRT
<213> Murinae gen. sp.

<400> 19
Ala Ser Val Leu Phe Lys Ala Glu Cys Asn Ile His Thr Ser Pro Ser
1 5 10 15

Pro Gly Ile Gln Val Arg His Val Tyr Thr Pro Ser Thr Thr Lys His
 20 25 30
 Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu Thr Asn Lys His Arg Gly
 35 40 45
 Asn Glu Val Ser Thr Thr Pro Leu Leu Ala Asn Ser Leu Ser Ala His
 50 55 60
 Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr Leu Ala Thr Arg Ile Glu
 65 70 75 80
 Gln Glu Asn Val Ile Asn His Thr Asp Glu Glu Gly Phe Thr Pro Leu
 85 90 95
 Met Trp Ala Ala Ala His Gly Gln Ile Ala Val Val Glu Phe Leu Leu
 100 105 110
 Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly Lys Gly Arg Glu Ser Ala
 115 120 125
 Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr Asp Ile Val Lys Met Leu
 130 135 140
 Leu Asp Cys Gly Val Asp Val Asn Glu Tyr Asp Trp Asn Gly Gly Thr
 145 150 155 160
 Pro Leu Leu Tyr Ala Gly His Gly Asn His Val Lys Cys Val Lys Met
 165 170 175
 Leu Leu Glu Asn Gly Ala Asp Pro Thr Ile Glu Thr Asp Ser Gly Tyr
 180 185 190
 Asn Ser Met Asp Leu Ala Val Ala Leu Gly Ile Glu Gly Cys Ser Asp
 195 200 205
 Tyr Met Leu Val Thr Asp Val Phe Arg Ile
 210 215

<210> 20

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FLAG epitope

<400> 20

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 21

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA promoter template

<400> 21

ggaccctttg caag

14

<210> 22

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA promoter template

<400> 22

tacatagcgt acgt

14

<210> 23

<211> 7

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA promoter template

<400> 23

tgcgta

7

<210> 24

<211> 7

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA promoter template

<400> 24

gacaagt

7